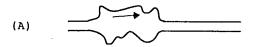


Figure 1 (A-F)

Construct Forms Comprising at Least one Single-Stranded Region











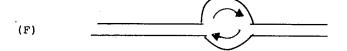
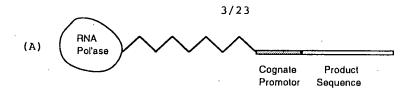
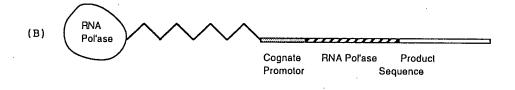


Figure 2 (A-F)

Functional Forms of the Construct





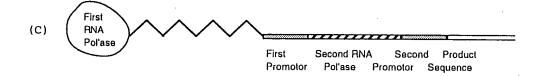


Figure 3 (A-C)

Three Constructs with an RNA Polymerase Covalently Attached to a Transcribing Cassette

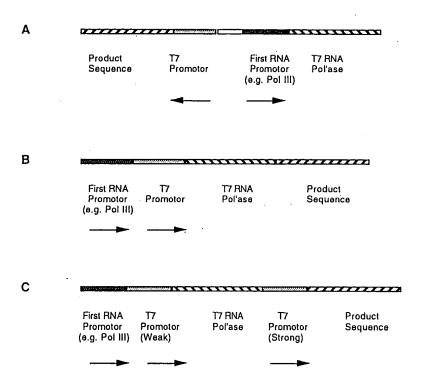


Figure 4 (A-C)

Three Constructs with Promoters for Endogenous RNA Polymerase

M13mp18. Seq Length: 7250

1.	AATGCTACTA	CTATTAGTAG	AATTGATGCC	ACCTTTTCAG	стозозос
51.	AAATGAAAAT	ATAGCTAAAC	AGGITATIGA	CCATTTGCGA	AATGTATCTA
101.	ATGGTCAAAC	TAAATCTACT	OGTTOGCAGA	ATTEGGAATC	AACTGTTACA
151.	TGGAATGAAA	CTTCCAGACA	COGTACTTTA	GTTGCATATT	TAAAACATGT
201	TGAGCTACAG	CACCAGATITC	AGCAATTAAG	CTCTAAGCCA	TOOGCAAAAA
251	TGACCTCTTA	TCAAAAGGAG	CAATTAAAGG	TACTCTCTAA	TOCTGACCTG
301.	TTGGAGTTTG	спосст	GGTTCGCTTT	GAAGCTOGAA	TTAAAACGCG
351.	ATATTTGAAG	TCTTTCGGGC	TTCCTCTTAA.	TCTTTTGAT	GCAATCCGCT
401.	TTCCTTCTCA	CTATAATAGT	CAGGGTAAAG	ACCTGATTTT	TGATTTATGG
451.	TCATTCTCGT	TTTCTGAACT	GTTTAAAGCA	TTTGAGGGGG	ATTCAATGAA
501.	TATTTATGAC	GATTOOGCAG	TATTOGACCC	TATCCAGTCT	AAACATTTTA
551.	CTATTACCCC	CTCTGGCAAA	ACTTCTTTTG	CAAAAGCCTC	TOGCTATTTT
601.	GGTTTTTATC	GICGICICGI	AAACGAGGGT	TATGATAGTG	TTGCTCTTAC
651.	TATGCCTCGT	AATTCCTTTT	GGCGTTATGT	ATCTGCATTA	GTTGAATGTG
701.	GTATTCCTAA	ATCTCAACTG	ATGAATCTTT	CTACCTGTAA	TAATGTTGTT
751.	COGTTAGTTC	GTTTTATTAA	CGTAGATTTT	TCTTCCCAAC	GTCCTGACTG
801.	GTATAATGAG	CCAGTTCTTA	AAATCGCATA	AGGTAATTCA	CAATGATTAA
851.	AGTTGAAATT	AAACCATCTC	AAGCCCAATT	TACTACTOGT	TCTCGTGTTC
901.	TOGTCAGGGC	AAGCTTATT	CACTGAATGA	CCACCTTTCT	TACGTTGATT
951.	TGGGTAATGA	ATATOOGGTT	CTTGTCGAAG	ATTACTCTTG	ATGAAGGTCA
1001	GCCAGCCTAT	GOOGOCT GGTC	TGTACACCGT	TCATCTGTCC	TCTTTCAAAG
1051	TTGGTCAGTT	COGTTCCCTT	ATGATTGACC	GTCTGCGCCT	COTTOCCECT
1101	AAGTAACATG	GAGCAGGTOG	CGGATTTCGA	CACAATTTAT	CAGGOGATGA
1151	TACAAATCTC	COTTOTACCTT	TGTTTCGCCGC	TTGGTATAAT	OCCIOCOCCIT
1201	CAAAGATGAG	TGTTTTAGTG	TATTCTTTCG	CCTCTTTCGT	TTTAGGTTGG

Figure 5

1251 TGOCTTOGTA GTGGCATTAC GTATTTTACC CGTTTAATGG AAACTTCCTC 1301 ATGAAAAAGT CTTTAGTCCT CAAAGCCTCT GTAGCCGTTG CTACCCTCGT 1351 TOOGATGCTG TCTTTOGCTG CTGAGGGTGA CGATOCOGCA AAAGOGGCCT 1401 TTAACTCCCT GCAAGCCTCA GCGACCGAAT ATATCGGTTA TOOGTOGGG 1451 ATGGTTGTTG TCATTGTCGG CGCAACTATC GGTATCAAGC TGTTTAAGAA 1501 ATTCACCTOG AAAGCAAGCT GATAAACCGA TACAATTAAA GGCTCCTTTT 1551 GGAGOCTTTT TTTTTGGAGA TTTTCAACGT GAAAAAATTA TTATTCGCAA 1601 TTCCTTTAGT TGTTCCTTTC TATTCTCACT COGCTGAAAC TGTTGAAAGT 1651 TGTTTAGCAA AACCCCATAC AGAAAATTCA TTTACTAACG TCTGGAAAGA 1701 CGACAAAACT TTAGATCGTT ACGCTAACTA TGAGGGTTGT CTGTGGAATG 1751 CTACAGGOGT TGTAGTTTGT ACTEGTGACG AAACTCAGTG TTACGGTACA 1801 TGGGTTCCTA TTGGGCTTGC TATCCCTGAA AATGAGGGTG GTGGCTCTGA 1851 GGGTGGCGGT TCTGAGGGTG GOOGTTCTGA GOGTGGOOGGT ACTAAACCTC 1901 CTGAGTACAG TGATACACCT ATTCCGGGCT ATACTTATAT CAACCCTCTC 1951 GACGICACTT ATCCGCCTGG TACTGAGCAA AACCCCCTA **ATCCTAATCC** 2001 TTCTCTTGAG GAGTCTCAGC CTCTTAATAC TTTCATGTTT CAGAATAATA 2051 GGTTCCGAAA TAGGCAGGGG GCATTAACTG TTTATACGGC CACTGTTACT 2101 CAAGGCACTG ACCOCGTTAA AACTTATTAC CAGTACACTC CTGTATCATC 2151 AAAAGOCATG TATGACGCTT ACTGGAACGG TAAATTCAGA GACTGCGCTT 2201 CAAGGCACTG ACCCCGTTAA AACTTATTAC CAGTACACTC CTGTATCATC 2151 AAAAGCCATG TGCCTCAACC TCCTGTCAAT GCTGGGGGGG GCTCTGGTGG 2201 TOCATTCTGG CTTTAATCAA GATCCATTCG TTTGTGAATA TCAAGGCCAA 2251 TOGTOTGACC TGCCTCAACC TCCTGTCAAT GCTGGCCGCG COTOTOGTICG 2301 TOGTTCTGGT COCCOCTCTG ACCCTCGGGCGC CTCTGAGCGT CCCCGGTTCTG 2351 AGGGTGGOGG CTCTGAGGGA GGOGGTTOOG GIGGIGGCIC TGGT1CCGGT 2401 GATITTGATT ATGAAAAGAT QQCAAACQCT AATAAGQQGG CTATGAQQGA 2451 AAATGOOGAT GAAAAOGOOC TACAGTCTGA OGCTAAAGGC AAACTTGATT

Figure 5

		•			
2501	CTGTCGCTAC	TGATTACGGT	<b>GCTGCTATCG</b>	ATGGTTTCAT	TEGTGACGIT
2551	TOOGGOOTTG	CTAATGGTAA	TOGTOCTACT	GGTGATTTTG	CTGGCTCTAA
2601	TTCCCAAATG	CCTCAAGTOG	GTGACGGTGA	TAATTCACCT	TTAATGAATA
2651	ATTTCCGTCA	ATATTTACCT	TOCCTOCCTC	AATOGGTTGA	ATGTCGCCCT
2701	TTTGTCTTTA	GOOCTOGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA
2751	AATAAACTTA	Посетеств	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT
2801	TTATGTATGT	ATTTTCTACG	TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT
2851	TTATCATGCC	AGTTCTTTTG	<b>GGTATTCCGT</b>	TATTATTGCG	TTTCCTCCGCT
2901	ПССПСТСС	TAACTTTGTT	COGCTATCTG	CTTACTTTTC	TTAAAAAGGG
2951	CTTCGGTAAG	ATAGCTATTG	CTATTTCATT	GTTTCTTGCT	CTTATTATTG
3001	<b>GGCTTAACTC</b>	AATTCTTGTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA
3051	COCTCTGACT	TIGTICAGGG	TGTTCAGTTA	ATTICTCCCGT	CTAATGCGCT
3101	TCCCTGTTTT	TATGTTATTC	TCTCTGTAAA	GECTECTATT	TTCATTTTTG
3151	ACGTTAAACA	AAAAATCGTT	TCTTATTTGG	ATTGGGATAA	ATAATATGGC
3201	TGTTTATTTT	GTAACTGGCA	AATTAGGCTC	TOGAMAGACG	CTCGTTAGCG
3251	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	<b>GGTGCAAAA</b> T	AGCAACTAAT
3301	CTTGATTTAA	GGCTTCAAAA	CCTCCCCGCAA	GTCCCCGACGT	TOGCTAAAAC
3351	COCTOCOCCTT	CTTAGAATAC	COGGATAAGOC	TTCTATATCT	GATTTGCTTG
3401	CTATTGGGGG	COGTAATGAT	TOCTACGAATG	AAAATAAAAA	ссесттестт
3451	GITCTCGATG	AGTGCCGTAC	TTGGTTTAAT	ACCOGTTCTT	GGAATGATAA
3501	GGAAAGACAG	COGATTATTG	ATTGGTTTCT	ACTOCTOGT	AAATTAGGAT
3551	GGGATATTAT	ппспеп	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG
3601	COTTICTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT
3651	TACTTTACCT	TTTGTCGGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA
3701	TEXCTICTEXC	TAAATTACAT	gilecocnic	TTAAATATGG	CGATTCTCAA
3751	TTAAGCCCTA	CTGTTGAGCG	TTGGCTTTAT	ACTOGTAAGA	ATTTGTATAA
3801	CGCATATGAT	ACTAAACAGG	CTTTTCTAG	TAATTATGAT	TCCGGTGTTT

Figure 5

3851 ATTOTTATTT AACGCCTTAT TTATCACACG GTOGGTATTT CAAACCATTA 3901 AATTTAGGTC AGAAGATGAA ATTAACTAAA ATAATATTGA AAAAGTTTTC 3951 TOGOGTTCTT TGTCTTGOGA TTGGATTTGC ATCAGCATTT ACATATAGTT 4001 ATATAACCCA ACCTAAGCCG GAGGTTAAAA AGGTAGTCTC TCAGACCTAT 4051 GATTITGATA AATTCACTAT TGACTCTTCT CAGCGTCTTA ATCTAAGCTA 4 1 0 1 TOGCTATGTT TTCAAGGATT CTAAGGGAAA ATTAATTAAT AGGGACGATT 4151 TACAGAAGCA AGGTTATTCA CTCACATATA TTGATTTATG TACTGTTTCC 4201 ATTAAAAAAG GTAATTCAAA TGAAATTGTT AAATGTAATT AATTTTGTTT 4251 TCTTGATGTT TGTTTCATCA TCTTCTTTTG CTCAGGTAAT TGAAATGAAT 4301 AATTOGOCTO TGOGOGATIT TGTAACITGG TATTCAAAGC AATCAGGOGA 4351 AATOCGTTATT GTTTCTCCCCG ATGTAAAACG TACTGTTACT GTATATTCAT 4401 CTGACGTTAA ACCTGAAAAT CTACGCAATT TCTTTATTTC TGTTTTACGT 4451 GCTAATAATT TTGATAATGGT TGGTTCAATT CCTTCCATAA TTCAGAAGTA 4501 TAATCCAAAC AATCAGGATT ATATTGATGA ATTGCCATCA TCTGATAATC 4551 AGGAATATGA TGATAATTCC CCTCCTTCTG GTGGTTTCTT TGTTCCGCAA 4601 AATGATAATG TTACTCAAAC TTTTAAAATT AATAACGTTC GGGCAAAGGA 4651 TITAATACGA GTIGTCGAAT IGTTTGTAAA GTCTAATACT TCTAAATCCT 4701 CAAATGTATT ATCTATTGAC GECTCTAATC TATTAGTTGT TAGTGCTCCT 4751 AAAGATATTT TAGATAACCT TCCTCAATTC CTTTCTACTG TTGATTTCCC 4801 AACTGACCAG ATATTGATTG AGGGTTTGAT ATTTGAGGTT CAGCAAGGTG 4851 ATGCTTTAGA TTTTTCATTT GCTGCTGGCT CTCAGOGTGG CACTGTTGCA 4901 GGOGGTGTTA ATACTGACOG CCTCACCTCT GTTTTATCTT 4951 TTCGTTCGGT ATTTTTAATG GCGATGTTTT AGGGCTTATCA GTTCGCCGCAT 5001 TAAAGACTAA TAGOCATTCA AAAATATTGT CTGTGOCACG TATTCTTACG 5051 CTTCAGGTC AGAAGGGTTC TATCTCTGTT GGCCAGAATG TCCCTTTTAT 5101 TAAAGACTAA TAGOCATTCA AAAATATTGT CTGTGOCACG TATTCTTACG 5151 CGATTGAGOG TCAAAATGTA GGTATTTCCA TGAGOGTTTT TCCTGTTGCA

-Figure 5

5201	ATGGCTGGCG -	GTAATATTGT	TCTGGATATT	ACCAGCAAGG	CCGATAGTTT
5251	GAGTTCTCT	ACTCAGGCAA	GTGATGTTAT	TACTAATCAA	AGAAGTATTG
5.301	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	COGTEGECCTC
5351	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGCGTACCGT	TOCTGTCTAA
5401	AATCCCTTTA	ATCGGCCTCC	TGTTTAGCTC	COGCTCTGAT	TOCAAOGAGG
5451	AAAGCACGTT	ATACGTGCTC	GTCAAAGCAA	CCATAGTACG	COCCTGTAG
5501	CCCCCCATTA	AGOGGGGGG	GIGIGGIGGI	TACGCGCAGC	GTGACCGCTA
5551	CACTTECCAG	COCCTAGCG	COOCCICCIT	TOGOTTTOTT	$\infty$ $\pi$
5601	CTCGCCACGIT	TOGOOGGCTT	TOCCOGTICAA	GCTCTAAATC	GEGEGETICCC
5651	TTTAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCGACCCC	AAAAAACTTG
5701	ATTTGGGTGA	TEGTTCACGT	AGTGGGCCAT	CCCCTGATA	GACGGTTTTT
5751	CGCCCTTTGA	CGTTCCAGTC	CACGITICITT	AATAGTGGAC	TCTTGTTCCA
5801	AACTGGAACA	ACACTCAACC	CTATCTCGGG	CTATTCTTTT	GATTTATAAG
5851	GGATTTTGCC	GATTTOGGAA	CCACCATCAA	ACAGGATTTT	CECCTECTEG
5901	GGCAAACCAG	OGTOGACCOCC	TTGCTGCAAC	TCTCTCAGGG	CCACCCCCTIG
5951	AAGGGCAATC	AGCTGTTGCC	OGICIOGCIG	GTGAAAAGAA	AAAOCACOCT
6001	GGCGCCCAAT	ACGCAAACCG	CTCTCCCCCG	COCCTTOCCC	GATTCATTAA
6051	TGCAGCTGGC	ACGACAGGIT	TOCOGACTEG	AAAGCCGGGCA	GTGAGCGCAA
6101	CGCAATTAAT	GTGAGTTAGC	TCACTCATTA	GGCACCCCAG	GCTTTACACT
6151	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	TTGTGAGCGG	ATAACAATTT
6201	CACACAGGAA	ACAGCTATGA	CCATGATTAC	GAATTOGAGC	TOGGTACCOG
6251	GOGATOCTCT	AGAGTOGACC	TECAGECATE	CAAGCTTGGC	ACTEGEOCGTC
6301	GTTTTACAAC	GTCGTGACTG	GGAAAACCCT	GGCGTTACCC	AACTTAATCG
6351	CCTTCCACCA	CAATCCCCTT	TOGOCAGCTG	GOGTAATAGC	GAAGAGGCCC
6401	CCACCCATCG	CCCTTCCCAA	CAGTTGCGCA	GOCTGAATGG	CGAATTGGCGC
6451	TITECCIEGI .	TTCCCGCACC	AGAAGOOGTIG	CCCGGAAAGCT	COCTOCACTG
6501	CGATCTTCCT	GAGGCCGATA	व्यवाद्याद्या	CCCCTCAAAC	TEGCAGATEC

Figure 5

6551	ACGGTTACGA	TGCGCCCATC	TACACCAACG	TAACCTATCC	CATTACGGTC
6601	AATCCCCCCCT	TIGITCCCAC	CCACAATOOG	ACCCGTTGTT	ACTOGCTCAC
6651	ATTTAATGTT	GATGAAAGCT	GGCTACAGGA	AGGCCAGACG	CGAATTATTT
6 7 <sup>.</sup> 0 1	TTGATGGOGT	TOCTATTOGT	TAAAAAATGA	GCTGATTTAA	CAAAAATTTA
6751	ACCCCAATTT	TAACAAAATA	TTAACGTTTA	CAATTTAAAT	ATTTGCTTAT
6801	ACAATCTTCC	TGTTTTGGG	COTTTICTGA	TTATCAACCG	GGGTACATAT
6851	GATTGACATG	CTAGTTTTAC	GATTACCGTT	CATCGATTCT	сттаттаст
6901	CCAGACTCTC	AGGICAATGAC	CTGATAGOCT	TTGTAGATCT	CTCAAAAATA
6951	CCTACCCTCT	COCCATGAA	TTTATCAGCT	AGAACGGTTG	AATATCATAT
7001	TGATGGTGAT	TTGACTGTCT		TCACCCTTTT	GAATCTTTAC
7051	CTACACATTA	CTCAGGCATT	GCATTTAAAA	TATATGAGGG	TTCTAAAAAT
7101	TTTTATCCTT	GCGTTGAAAT	AAAGGCTTCT	CCCCCAAAAG	TATTACAGGG
7151	TCATAATGTT	TTTGGTACAA	COGATTTAGC	TTTATGCTCT	GAGGCTTTAT

Figure 5

# COMPLEMENTARY TO M<sub>13</sub>

POSITION 6 4 5	5' 3' AGCAACACTATCATÁ	POSITION 631	M <sub>13</sub> /1
615	ACGACGATAAAAACC	601	M <sub>13</sub> /2
585	TTTTGCAAAAGAAGT	571	M <sub>13</sub> /3
555	AATAGTAAAATGTTT	541	M <sub>13</sub> /4
525	CAATACTGCGGAATG	511	M <sub>13</sub> /5
495	TGAATCCCCCTCAAA	481	M <sub>13</sub> /6
465	AGAAAACGAGAATGA	451	M <sub>13</sub> /7
435	CAGGTCTTTACCCTG	421	M <sub>13</sub> /8
405	AGGAAAGOGGATTGC	391	M <sub>13</sub> /9
375	AGGAAGOOOGAAAGA	361	M <sub>13</sub> /10

### COMPLEMENTARY TO SS PHAGE DNA

POSITION	5' * * 3'	POSITION	
351	ATATTTGAAGTCTTT	366	M <sub>13</sub> /11
371	TCTTTTTGATGCAAT	386	M <sub>13</sub> /12
391	CTATAATACTCAGGG	406	M <sub>13</sub> /13
411	TGATTTATGGTCATT	426	M <sub>13</sub> /14
431	GTTTAAAGCATTTGA	4 4 6	M <sub>13</sub> /15
451	TATTTATGACGATTC	466	M <sub>13</sub> /16
471	TATCCAGTCTAAACA	486	M <sub>13</sub> /17
491	CTCTGGCAAAACTTC	506	M <sub>13</sub> /18
511	TCGCTATTTTGGTTT	526	M <sub>13</sub> /19
531	AAAOGAGGGTTATGA	546	M <sub>13/2</sub> 0

Figure 6

Primers for Nucleic Acid Production Derived from M13mp18 Sequence

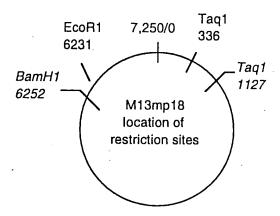


Figure 7

Appropriate M13mp18 Restriction Sites



Lane 1: from calf thymus + Taq digested mp18 amplification reaction

Lane 2: from Taq digested mp18 amplification reaction

Lane 3: from calf thymus amplification reaction

Lane 4: øX174 Hinf1 size marker

Figure 8

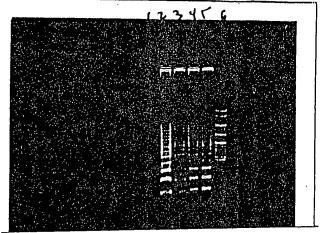


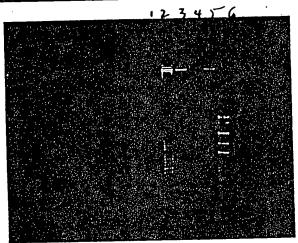
Lane 1: no template

Lane 2: mp18 template, phosphate buffer

Lane 3: Mspl/pBR322 size marker Lane 4: mp18 template, MOPS buffer

Figure 9





Top= (+) Template
Bottom= (-) Template

Lane 1: phosphate buffer

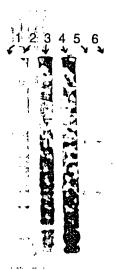
Lane 2: MES

Lane 3: MOPS

Lane 4: DMAB

Lane 5: DMG

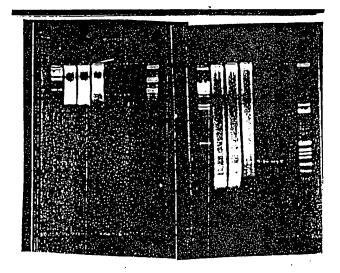
Lane 6: pBR322/Mspl size marker



Lane 1: DMAB buffer, no template Lane 2: DMAB buffer, mp18 template Lane 3: DMG buffer, no template Lane 4: DMG buffer, mp18 template Lane 5: No reaction

Lane 6: 200 ng Taq I digested mp18 size marker/positive control

Figure 11



First Time Interval Second Time Interval

## Agarose Gel Analysis

- Lane 1: lambda Hind III marker
- Lane 2: Amp/Untreated
- Lane 3: Amp/Kinased
- Lane 4: Amp/Kinased/Ligated
- Lane 5: PCR/Untreated
- Lane 6: PCR/Kinased
- Lane 7: PCR/Kinased/Ligated
- Lane 8: øX174/Hinf1 marker

18/23

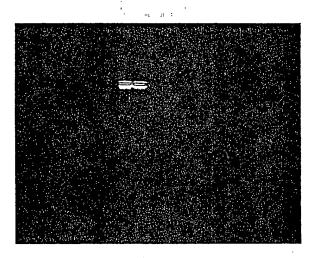
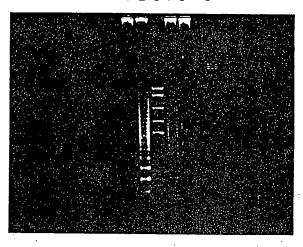


Figure 13

19/23

1 2 3 4 5



Lane 1: Primers alone

Lane 2: Primers + taq digested M13 DNA

Lane 3: Molecular weight markers

Lane 4: Primers + RNA

Lane 5: Primers alone

Lane 6: M13 digested DNA

Buffer was dimethyl amino glycine, pH 8.6

Figure 14



Lane 1: Primers alone

Lane 2: Primers + taq digested M13 DNA

Lane 3: Molecular weight markers

Lane 4: Primers + RNA

Lane 5: Primers alone

Lane 6: M13 digested DNA

Buffer was dimethyl amino glycine, pH 8.6

Figure 15

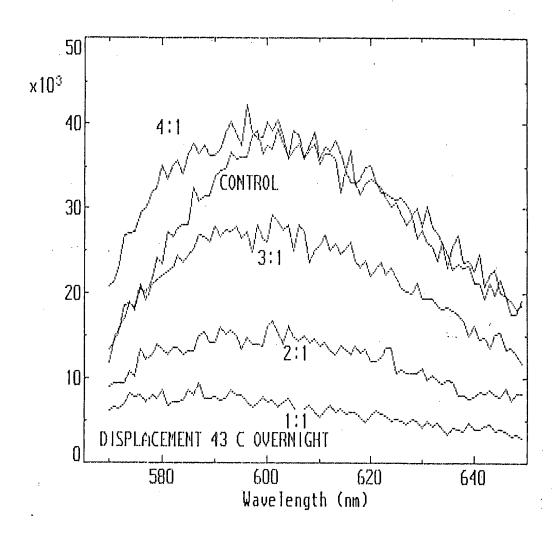


Figure 16

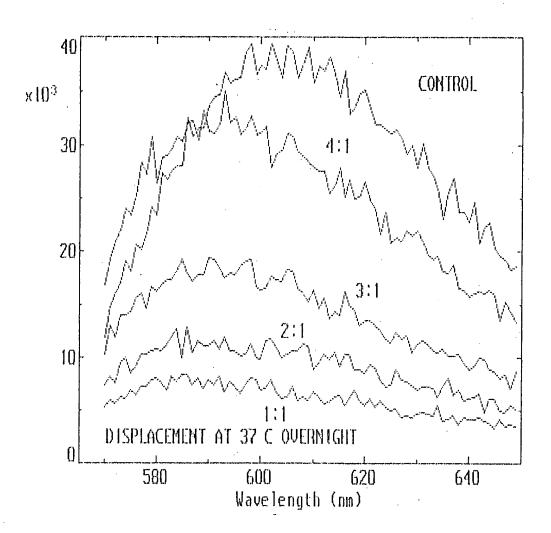


Figure 17

#### 23/23

## plBI 31-BH5-2

fmet AUG of Lac z {T7 Promotor region.... LAC PROMOTOR.ATG ACC ATG ATT ACG CCA GAT ATC AAA TTA ATA CGA CTC ACT ATA

oligo 50-mer

3'- tac t\*aa t\*gc ggt\* ct\*a t\*ag t\*Vt aat\* tat\* gct\* gag t\*ga t\*at\* c-5' 10 base insert

T7 RNA Start («« T3 Promotor Region ) IGGG CTC ICCT TTA GTG ACG GTT AAT ....»») «- T3 Start Signal

## pIBI 31 BSII/HCV

(«- T7 Promotor Region )

MULTIPLE CLONING SITE + 390 BASE INSERT CTA /TAG TGA GTC CGT ATT AAT....

«- T7 Start Signal

5'-ct'a t'ag t'ga gt'c gt'a tt'a at'..........